

RESULT 1  
US-09-745-763-35  
Sequence 35, Application US/09745763  
Patent No. US20020065394A1  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
McCoy, John M.  
Lavaille, Edward R.  
Collins-Racie, Lisa A.  
Evans, Cheryl  
Merberg, David  
Treacy, Maurice  
Spaulding, Vikki  
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES  
ENCODING THEM  
NUMBER OF SEQUENCES: 219  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02140

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/745,763  
 FILING DATE: 18-Jun-2000  
 CLASSIFICATION: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sprunger, Suzanne A.  
 REGISTRATION NUMBER: 41,323  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 498-8284  
 TELEFAX: (617) 876-5851  
 INFORMATION FOR SEQ ID NO: 35:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1851 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
 US-09-745-763-35  
 Alignment Scores:  
 Pred. No.: 3,72e-289 Length: 1851  
 Score: 2417.00 Matches: 472  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0  
 US-09-745-763-36 (1-472) x US-09-745-763-35 (1-1851)

639 TCAGAGCGGTGCAATACCGAACGAGGCGGTGGAGGCTGCCAAGTGGGGCTTTG 698  
 QY AlaSerLeuIleArgSerValAlaSerPheSerIleTyrSerProHisThrGlyIleGln 220  
 DB GCATCTCATTCATTCATCCGTGGCTCTCTCCATCTCAACATCTCTCCACAGGAAATTCAG 758  
 QY GluTyrGlnAspGlyValProLysIleProThrAlaCysIleThrValGluAspAlaGlu 240  
 DB GAATTCAGAGATGGCGTGGCCCAAAATTCCAACAGCTGTATTACGTGGAGAAATGCAAA 818  
 QY 759 GAATTCAGAGATGGCGTGGCCCAAAATTCCAACAGCTGTATTACGTGGAGAAATGCAAA 818  
 DB 241 MetMetSerArgMetAlaSerHisGlyIleLysIleValIleGlnLeuLysMetGlyVal 260  
 QY 819 ATGATGTCAGAAATGCGCTTCCATGGATCAAAATTCATTCAGTCACTAAAGATGGGGCA 878  
 DB 261 LysThrTyrProAspThrAspSerPheAsnThrValAlaGluIleThrGlySerLysTyr 280  
 QY 879 AAGACCTACCCAGATGATGATCTCTTCAACACCTGACAGAGATCACTGGAGCAAAATAT 938  
 DB 281 ProGluGlnValValLeuValSerGlyHisIleuAspSerThrAspValGlyGlnGlyVal 300  
 QY 939 CCAGAACAGGTTGATCGTTCAGTGCAGATCTGCAGACGCTGGAGATGTTGGCAGAGGTC 998  
 DB 301 MetAspAspGlyGlyGlyAlaPheIleSerTyrGluAlaLeuSerLeuIleLysAspLeu 320  
 QY 999 ATGATGATGCGCGGTGAGGCTTATATCATGGAGACACTCTCATTTATTAAGATCTT 1058  
 DB 321 GlyLeuArgProLysArgThrLeuArgLeuValLeuThrPheIleGluGlnGlyGly 340  
 QY 1059 GGGCTGCTCCAAAGAGACCTGCGGCTGTGTCTGCACTGCACTGCAAGAAACAGGTGGA 1118  
 DB 341 ValGlyAlaPheGlnTyrTyrGlnLeuHisValAsnIleSerAsnTyrSerLeuVal 360  
 QY 1119 GTTGATGCTTCCAGATATATCATGTTTCAACAGGTAATTTTCCACTACATGCTGCTG 1178  
 DB 361 MetGluSerAspAlaGlyThrPheLeuProThrGlyLeuGlnPheThrGlySerGlyLys 380  
 QY 1179 ATGAGCTGACCGACGAGAACCTTCTTACCACTGCGGCTGCATTCACCTGCAAGAAAG 1238  
 DB 381 AlaArgAlaIleMetGluGlnValMetSerLeuGlnProLeuAsnIleThrGlnVal 400  
 QY 1239 GCCAGGCGCATCATGAGAGGTTATGAGCTGTGCTGACGCCCTCATATCATCTCAGGTC 1298  
 DB 401 LeuSerHisGlyGlnGlyThrAspIleAsnPheTyrIleGlnAlaGlyValProGlyVal 420  
 QY 1299 CTGAGCCATGAGAGAGAGACAGACATCACTTTGGATCCAACTGAGTGGCTGAGGCC 1358  
 DB 421 SerLeuLeuAspAspLeuTyrLysTyrPhePhePheHisSerHisGlyAspThrMet 440  
 QY 1359 AGTCTACTGATGACTTATACAGATATTTCTTCTTCATCATCATCCACGAGACACCATG 1418  
 DB 441 ThrValMetAspProLysGlnMetAsnValAlaAlaAlaValThrAlaValValSerTyr 460  
 QY 1419 ACTGTATGATTCAAAGACAGATGATGATGCTGCTGCTGTGGCTGTGGCTGTGTTCTTAT 1478  
 DB 461 ValValAlaAspMetGluGlnMetLeuProArgSer 472  
 QY 1479 GTTGTTCAGACATGAGAAATGCTGCTAGGTCC 1514  
 DB